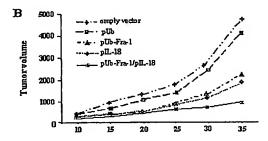


FIG. 1

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A
Suppression of lung metastases of D2F2 by oral DNA vaccine

Treatment groups	Metastasis Score							
A. Empty vector	23333333							
B. pUb	33333333							
C.pUb-Fra-l	11222223							
D.pIL-18	00111222							
E.pUb-Fra-1/plL-18	00000112							



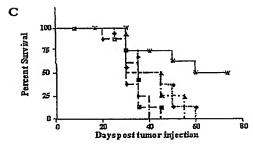


FIG. 2

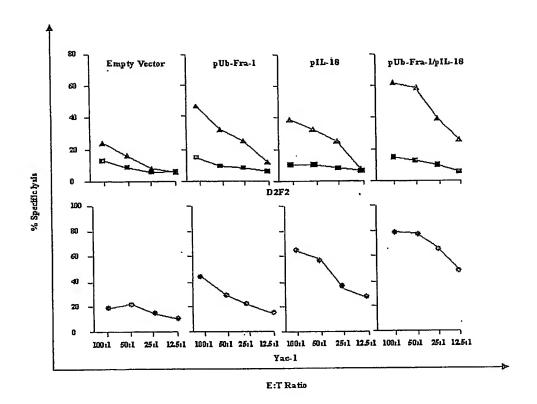


FIG. 3

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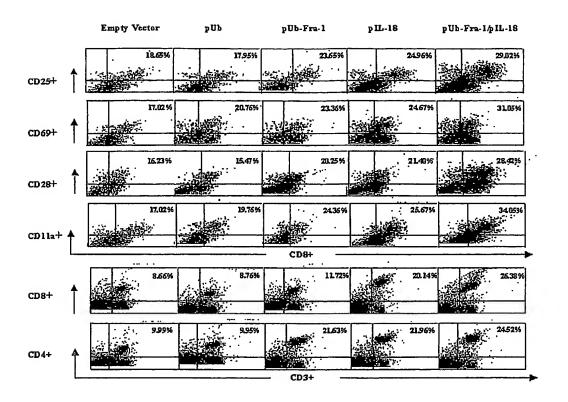


FIG. 4

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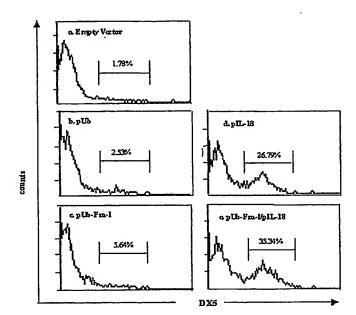


FIG. 5

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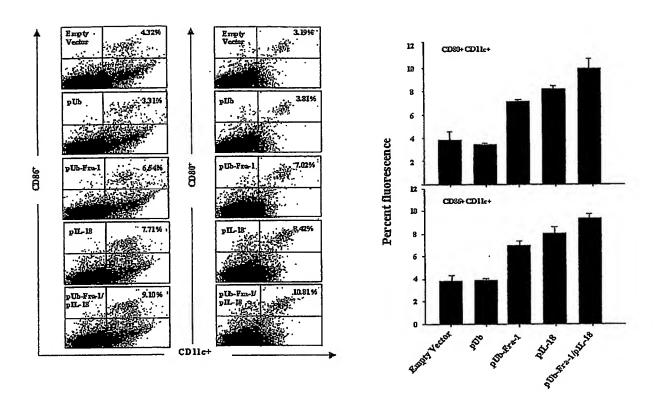


FIG. 6

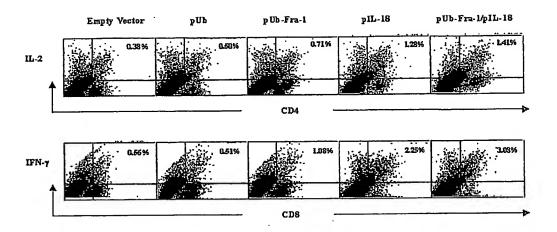


FIG. 7

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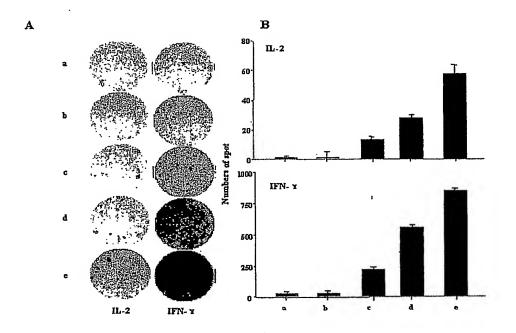


FIG. 8

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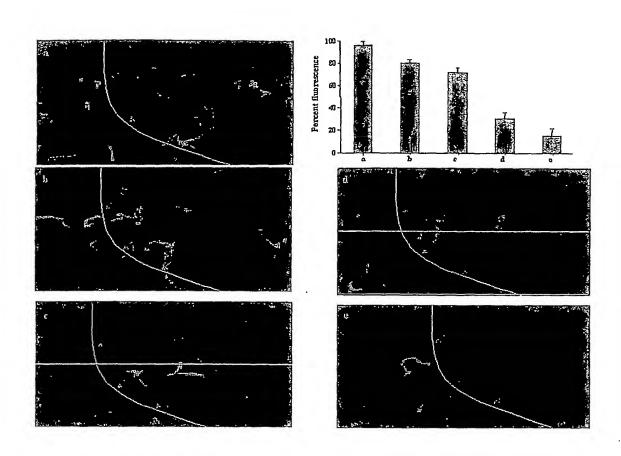


FIG. 9.

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Homo sapiens - Fra-1

VERSION NM_005438.1 GI:4885242

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Homo sapiens - Fra-1

MFRDFGEPGPSSGNGGGYGGPAQPPAAAQAAQQKFHLVPSINTMSGSQELQWMVQPHFLGPSSYPRPLTY PQYSPPQPRPGVIRALGPPPGVRRRPCEQISPEEEERRRVRRERNKLAAAKCRNRRKELTDFLQAETDKL EDEKSGLQREIEELQKQKERLELVLEAHRPICKIPEGAKEGDTGSTSGTSSPPAPCRPVPCISLSPGPVL EPEALHTPTLMTTPSLTPFTPSLVFTYPSTPEPCASAHRKSSSSSGDPSSDPLGSPTLLAL (SEO ID NO: 2)

Murine Fra-1

(DNA Sequence, SEQ ID NO: 3; Protein Sequence, SEQ ID NO: 4) 1 ATGTACCGAGACTACGGGGACCGGGACCGGGGCTGGCAGCGCGTACGGTCGC 60 1 M Y R D Y G E P G P S S G A G S A Y G R 20 61 CCCGCGCAGCCCCGCAAGCTCAGGCACAGACCGCCCAGCAGCAGAAGTTCCACTTTGTG 120 21 PAQPPQAQAQTAQQQKFHFV 121 CCAAGCATCGACAGCAGCAGCAGGAACTGCACTGGATGGTGCAGCCTCATTTCCTGGGA 41 P S I D S S S Q E L H W M V O P H F L G 60 181 CCCACTGGCTATCCCCGACCTCTGGCCTATCCCCAGTACAGTCCCCCTCAGCCCCGGCCA 240 61 P T G Y P R P L A Y P Q Y S P P Q P R P 80 241 GGAGTCATACGAGCCCTAGGGCCACCTCCGGGGGTGCGTCGCAGGCCCTGCGAGCAGATC 300 81 G V I R A L G P P P G V R R P C E O I 301 AGCCCAGAGGAGGAAGAGCGCCGCAGGGTGAGACGAGCGGAACAAGCTAGCAGCTGCT 101 S P E E E R R R V R R E R N K L A A A 361 AAGTGCAGAAACCGAAGAAAGGAGCTGACAGACTTCCTGCAGGCGGAGACCGACAAATTG 420 121 K C R N R R K E L T D F L Q A E T D K L 421 GAGGATGAGAAATCGGGGCTGCAGCGAGAGATTGAAGAGCTGCAGAAGCAGAAGGAACGC 480 141 E D E K S G L Q R E I E E L Q K Q K E R 481 CTTGAGCTGGTGCTGGAAGCCCATCGCCTCATCTGCAAAATCCCAGAAGGAGACAAGAAG 540 161 L E L V L E A H R L I C K I P E G D K K 180 541 GACCCAGGTGTTCTGGCAGCACCAGCGGGGCTAGCAGCCCACCAGCCCCGGCCGCCCA 600 181 D P G G S G S T S G A S S P P A P G R P 200 601 GTGCCTTGCATCTCCCTTTCTCCAGGACCCGTACTTGAACCGGAAGCACTGCATACCCCC 660 201 V P C I S L S P G P V L E P E A L H T P 220 661 ACGCTCATGACCACCCTCTCTGACTCCTTTTACTCCGAGTCTGGTTTTCACCTATCCT 720 221 T L M T T P S L T P F T P S L V F T Y P 240 721 AGCACACCAGAACCTTGCTCCTCCACTCACCGAAAGAGTAGCAGCAGCAGTGGCGACCCC 241 S T P E P C S S T H R K S S S S G D P 781 TCCTCCGACCCCTGGGCTCTCCTACACTCCTGGCTTTGTGA 822 261 S S D P L G S P T L L A L * 274

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Homo sapiens - IL-18

VERSION NM 001562.2 GI:27502389

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1 attetece cagettgetg ageeetttge teecetggeg actgetgga cagteagea fl ggaattget ceeagtgat tttgeeetee tggetgeaa etetggetge taaagegget ggaacteaga etetggetget taaagegget ggaeetteete geagtetaea cagetteggg aggaataaag gaaceteaga eetetgat aggaeattge ateaacttg tggeaatgaa atttattgae attattgee attggeaga atttattgae ettggaatga aattattgae ettgaateta aattategge ettgaateta aggaatatgge etgaagataa tgeeageegg etgaagataa teeggata ettetgae etgaagata teeggaagata teeggaagata ettetgae etgaagata etetggaagatae etetggaagatae etetggaagatae etetggaagatae etetggaagatae etetgaagatae etetg
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Homo sapiens - IL-18

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Murine IL-18 (DNA Sequence, SEQ ID NO: 7; Protein Sequence, SEQ ID NO: 8)

ATG	GCT	GCC.	ATG'	TCA	GAA:	GAC'	rct'	TGC	GTC	AAC	TTC	AAG	gaa	ATG	ATG	${f TTT}$	ATT	GAC.	AAC	60
M	A	A	M	S	E	D	S	С	V	N	F	K	E	М	M	F	I	D	N	20
ACG	CTT	TAC'	TTT	ATA	CCT	GAA	GAA	AAT	GGA	GAC	CTG	GAA	TCA	GAC	AAC	TTT	GGC	CGA	CTT	120
T	L	Y	F	I	P	E	E	N	G	D	L	E	S	D	N	F	G	R	L	40
CAC	TGT	ACA.	ACC	GCA	GTA	ATA	CGG.	AAT.	ATA	AAT	GAC	CAA	GTT	CTC	TTC	GTT	GAC	AAA	AGA	180
H	С	T	T	A	V	I	R	N	I	N	D	Q	V	L	F	V	D	K	R	60
CAG	ССТ	GTG	TTC	GAG	GAT.	ATG	ACT	GAT.	АТТ	GAT	CAA	AGT	GCC	AGT	GAA	.ccc	CAG	ACC	AGA	240
Q	P	V	F	E	D	M	T	D	I	D	Q	S	A	S	E	P	Q	T	R	80
CTG	ATA	ATA	TAC	ATG	TAC	AAA	GAC.	AGT	GAA	GTA	AGA	.GGA	CTG	GCT	GTG	ACC	CTC	TCT	GTG	300
L	Ι	I	Y	M	Y	K	D.	S	E	V	R	G	L	A	V	. Т	L	s	V	100
AAG	GAT	AGT.	AAA	ATG	TCT.	ACC	CTC	TCC	TGT	AAG	AAC	AAG	ATC	ATT	TCC	TTT	'GAG	GAA	ATG	360
K	D	s	K	M	s	T	L	s	С	K	N	K	I	I	S	F	E	E	M	120
GAT	CCA	CCT	GAA	AAT.	ATT	GAT	GAT.	ATA	CAA	AGT	GAT	CTC	ATA	TTC	TTT	CAG	AAA	CGT	GTT	420
D	P	P	E	N	I	D	D	I	Q	s	D	L	I	F	F	Q	K	R	v	140
CCA	GGA	CAC	AAC	AAG.	ATG	GAG	TTT	GAA	TCT	TCA	CTG	TAT	GAA	.GGA	CAC	TTT	CTT	GCT	TGC	480
P	G.	Н	N	K	М	E	F	E	S	S	L	Y	E	G	Н	F	Г	A	С	160
CAA	AAG	GAA	GAT	GAT	GCT	TTC.	AAA	CTC	ATT	CTG	AAA	AAA	AAG	GAT	'GAA	AAT	'GGG	GAT	AAA	540
. Q	K	E	D	D	A	F	K	L	I	L	K	K	K	D	E	N	G	D	K	180
TCT	GTA	ATG	TTC.	ACT	CTC	ACT.	AAC	TTA	CAT	CAA	AGT	TAG								579
s	V	M	F	T	L	T	N	${f L}$	H	Q	s	*								193
	M ACG T CAC H CAG Q CTG L AAG K GAT D CCA P CAA	M A ACGCTT T L CACTGT H C CAGCCT Q P CTGATA L I AAGGAT K D GATCCA D P CCAGGA P G CAAAAG Q K TCTGTA	M A A ACGCTTTAC T L Y CACTGTACA H C T CAGCCTGTG Q P V CTGATAATA L I I AAGGATAGT K D S GATCCACCT D P P CCAGGACAC P G H CAAAAGGAA Q K E TCTGTAATG	M A A M ACGCTTTACTTT. T L Y F CACTGTACAACC H C T T CAGCCTGTGTTC Q P V F CTGATAATATAC L I I Y AAGGATAGTAAA K D S K GATCCACCTGAA D P P E CCAGGACACAAC P G H N CAAAAGGAAGAT Q K E D TCTGTAATGTTC	M A A M S ACGCTTTACTTTATAGE T L Y F I CACTGTACAACCGCAGE H C T T A CAGCCTGTGTTCGAGE Q P V F E CTGATAATATACATG L I I Y M AAGGATAGTAAAATG K D S K M GATCCACCTGAAAAT D P P E N CCAGGACACAACAAG P G H N K CAAAAGGAAGATGAT Q K E D D TCTGTAATGTTCACT	M A A M S E ACGCTTTACTTTATACCT T L Y F I P CACTGTACAACCGCAGTA H C T T A V CAGCCTGTGTTCGAGGAT Q P V F E D CTGATAATATACATGTAC L I I Y M Y AAGGATAGTAAAATGTCT K D S K M S GATCCACCTGAAAATATT D P P E N I CCAGGACACAACAAGATG P G H N K M CAAAAGGAAGATGATGCT Q K E D D A TCTGTAATGTTCACTCTC	M A A M S E D ACGCTTTACTTTATACCTGAA T L Y F I P E CACTGTACAACCGCAGTAATA H C T T A V I CAGCCTGTGTTCGAGGATATG Q P V F E D M CTGATAATATACATGTACAAA L I I Y M Y K AAGGATAGTAAAATGTCTACC K D S K M S T GATCCACCTGAAAATATTGAT D P P E N I D CCAGGACACAACAAGATGGAG P G H N K M E CAAAAGGAAGATGATGATC Q K E D D A F TCTGTAATGTTCACTCTCACT	M A A M S E D S ACGCTTTACTTTATACCTGAAGAA T L Y F I P E E CACTGTACAACCGCAGTAATACGG. H C T T A V I R CAGCCTGTGTTCGAGGATATGACT Q P V F E D M T CTGATAATATACATGTACAAAGAC L I I Y M Y K D AAGGATAGTAAAATGTCTACCCTC K D S K M S T L GATCCACCTGAAAATATTGATGAT D P P E N I D D CCAGGACACAACAAGATGAGTTT P G H N K M E F CAAAAGGAAGATGATGATGTCTACAA Q K E D D A F K TCTGTAATGTTCACTCTCACTAAC	M A A M S E D S C ACGCTTTACTTTATACCTGAAGAAAAT T L Y F I P E E N CACTGTACAACCGCAGTAATACGGAAT. H C T T A V I R N CAGCCTGTGTTCGAGGATATGACTGAT. Q P V F E D M T D CTGATAATATACATGTACAAAGACAGT. L I I Y M Y K D S AAGGATAGTAAAATGTCTACCCTCTCC K D S K M S T L S GATCCACCTGAAAATATTGATGATATA D P P E N I D D I CCAGGACACAACAAGATGGAGTTTGAA P G H N K M E F E CAAAAGGAAGATGATGCTTCAAACTC Q K E D D A F K L TCTGTAATGTTCACTCTCACTAACTTA	M A A M S E D S C V ACGCTTTACTTTATACCTGAAGAAAATGGA T L Y F I P E E N G CACTGTACAACCGCAGTAATACGGAATATA H C T T A V I R N I CAGCCTGTGTTCGAGGATATGACTGATATT Q P V F E D M T D I CTGATAATATACATGTACAAAGACAGTGAA L I I Y M Y K D S E AAGGATAGTAAAATGTCTACCCTCTCTGT K D S K M S T L S C GATCCACCTGAAAATATTGATGATATACAA D P P E N I D D I Q CCAGGACACAACAAGATGGAGTTTGAATCT P G H N K M E F E S CAAAAGGAAGATGATGCTTTCAAACTCATT Q K E D D A F K L I TCTGTAATGTTCACCTCTCACTACTT	M A A M S E D S C V N ACGCTTTACTTTATACCTGAAGAAAATGGAGAC T L Y F I P E E N G D CACTGTACAACCGCAGTAATACGGAATATAAAT H C T T A V I R N I N CAGCCTGTGTTCGAGGATATGACTGATATTGAT Q P V F E D M T D I D CTGATAATATACATGTACAAAGACAGTGAAGTA L I I Y M Y K D S E V AAGGATAGTAAAATGTCTACCCTCTCTGTAAG K D S K M S T L S C K GATCCACCTGAAAATATTGATGATATACAAAGT D P P E N I D D I Q S CCAGGACACAACAAGATGGAGTTTGAATCTCA P G H N K M E F E S S CAAAAGGAAGATGATGCTTTCAAACTCATTCTG Q K E D D A F K L I L TCTGTAATGTTCACTCTCACTAACTTACATCAA	M A A M S E D S C V N F ACGCTTTACTTTATACCTGAAGAAAATGGAGACCTG T L Y F I P E E N G D L CACTGTACAACCGCAGTAATACGGAATATAAATGAC H C T T A V I R N I N D CAGCCTGTGTTCGAGGATATGACTGATATTGATCAA Q P V F E D M T D I D Q CTGATAATATACATGTACAAAGACAGTGAAGTAAGA L I I Y M Y K D S E V R AAGGATAGTAAAATGTCTACCCTCTCTGTAAGAAC K D S K M S T L S C K N GATCCACCTGAAAATATTGATGATATACAAAGTGAT D P P E N I D D I Q S D CCAGGACACAACAAGATGGAGTTTGAATCTTCACTG P G H N K M E F E S S L CAAAAGGAAGATGATGCTTTCAAACTCATCTGAAA Q K E D D A F K L I L K TCTGTAATGTTCACTCTCACTAACTTACATCAAAGT	M A A M S E D S C V N F K ACGCTTTACTTTATACCTGAAGAAAATGGAGACCTGGAA T L Y F I P E E N G D L E CACTGTACAACCGCAGTAATACGGAATATAAATGACCAA H C T T A V I R N I N D Q CAGCCTGTGTTCGAGGATATGACTGATATTGATCAAAGT Q P V F E D M T D I D Q S CTGATAATATACATGTACAAAGACAGTGAAGTAAGAGGA L I I Y M Y K D S E V R G AAGGATAGTAAAATGTCTACCCTCTCCTGTAAGAACAAG K D S K M S T L S C K N K GATCCACCTGAAAATATTGATGATATACAAAGTGATCTC D P P E N I D D I Q S D L CCAGGACACAACAAGATGGAGTTTGAATCTTCACTGTAT P G H N K M E F E S S L Y CAAAAGGAAGATGATGCTTTCAAACTCATCTGAAAAAA Q K E D D A F K L I L K K TCTGTAATGTTCACTCTCACTAACTTACAAAGTTAG	M A A M S E D S C V N F K E ACGCTTTACTTTATACCTGAAGAAAATGGAGACCTGGAATCA T L Y F I P E E N G D L E S CACTGTACAACCGCAGTAATACGGAATATAAATGACCAAGTT H C T T A V I R N I N D Q V CAGCCTGTGTTCGAGGATATGACTGATATTGATCAAAGTGCC Q P V F E D M T D I D Q S A CTGATAATATACATGTACAAAGACAGTGAAGTAAGAGGACTG L I I Y M Y K D S E V R G L AAGGATAGTAAAATGTCTACCCTCTCCTGTAAGAACAAGATC K D S K M S T L S C K N K I GATCCACCTGAAAATATTGATGATATACAAAGTGATCTCATA D P P E N I D D I Q S D L I CCAGGACACAACAAGATGGAGTTTGAATCTTCACTGTATGAA P G H N K M E F E S S L Y E CAAAAGGAAGATGATGCTTTCAAACTCATCTAAAAAAAAA	M A A M S E D S C V N F K E M ACGCTTTACTTTATACCTGAAGAAAATGGAGACCTGGAATCAGAC T L Y F I P E E N G D L E S D CACTGTACAACCGCAGTAATACGGAATATAAATGACCAAGTTCTC H C T T A V I R N I N D Q V L CAGCCTGTGTTCGAGGATATGACTGATATTGATCAAAGTGCCAGT Q P V F E D M T D I D Q S A S CTGATAATATACATGTACAAAGACAGTGAAGTAAGAGGACTGGCT L I I Y M Y K D S E V R G L A AAGGATAGTAAAATGTCTACCCTCTCCTGTAAGAACAAGATCATT K D S K M S T L S C K N K I I GATCCACCTGAAAATATTGATGATATACAAAGTGATCTCATATTC D P P E N I D D I Q S D L I F CCAGGACACAACAAGATGGAGTTTGAATCTTCACTGTATGAAGGA P G H N K M E F E S S L Y E G CAAAAGGAAGATGATGCTTTCAAACTCATTCTGAAAAAAAA	M A A M S E D S C V N F K E M M ACGCTTTACTTTATACCTGAAGAAAATGGAGACCTGGAATCAGACAAC T L Y F I P E E N G D L E S D N CACTGTACAACCGCAGTAATACGGAATATAAATGACCAAGTTCTCTTC H C T T A V I R N I N D Q V L F CAGCCTGTGTTCGAGGATATGACTGATATTGATCAAAGTGCCAGTGAA Q P V F E D M T D I D Q S A S E CTGATAATATACATGTACAAAGACAGTGAAGTAAGAGGACTGGCTGTG L I I Y M Y K D S E V R G L A V AAGGATAGTAAAATGTCTACCCTCTCTGTAAGAACAAGATCATTTCC K D S K M S T L S C K N K I I S GATCCACCTGAAAATATTGATGATATACAAAGTGATCTCATATTCTTT D P P E N I D D I Q S D L I F F CCAGGACACAACAAGATGAGTTTGAATCTTCACTGTATGAAGGACAC P G H N K M E F E S S L Y E G H CAAAAGGAAGATGATGCTTTCAAACTCATCTAAAAAAAAA	M A A M S E D S C V N F K E M M F ACGCTTTACTTTATACCTGAAGAAAATGGAGACCTGGAATCAGACAACTTT T L Y F I P E E N G D L E S D N F CACTGTACAACCGCAGTAATACGGAATATAAATGACCAAGTTCTCTTCGTT H C T T A V I R N I N D Q V L F V CAGCCTGTGTTCGAGGATATGACTGATATTGATCAAAGTGCCAGTGAACCC Q P V F E D M T D I D Q S A S E P CTGATAATATACATGTACAAAGACAGTGAAGTAAGAGGACTGGCTGTGACC L I I Y M Y K D S E V R G L A V T AAGGATAGTAAAATGTCTACCCTCTCTGTAAGAACAAGATCATTTCCTTT K D S K M S T L S C K N K I I S F GATCCACCTGAAAATATTGATGATATACAAAGTGATCTCATATTCTTTCAG D P P E N I D D I Q S D L I F F Q CCAGGACACAACAAGATGGAGTTGAATCTTCACTGTATGAAGGACACTTT P G H N K M E F E S S L Y E G H F CAAAAAGGAAGATGATGCTTTCAAACTCATTCTGAAAAAAAA	M A A M S E D S C V N F K E M M F I ACGCTTTACTTTATACCTGAAGAAAATGGAGACCTGGAATCAGACAACTTTGGC T L Y F I P E E N G D L E S D N F G CACTGTACAACCGCAGTAATACGGAATATAAATGACCAAGTTCTCTTCGTTGAC H C T T A V I R N I N D Q V L F V D CAGCCTGTGTTCGAGGATATGACTGATATTGATCAAAGTGCCAGTGAACCCCAG Q P V F E D M T D I D Q S A S E P Q CTGATAATATACATGTACAAAGACAGTGAAGTAAGAGGACTGGCTGTGACCCTC L I I Y M Y K D S E V R G L A V T L AAGGATAGTAAAATGTCTACCCTCTCCTGTAAGAACAAGATCATTTCCTTTGAG K D S K M S T L S C K N K I I S F E GATCCACCTGAAAATATTGATGATATACAAAGTGATCTCATATTCTTTCAGAAA D P P E N I D D I Q S D L I F F Q K CCAGGACACAACAAGATGGAGTTTGAATCTTCACTGTATGAAGACACTTTCTT P G H N K M E F E S S L Y E G H F L CAAAAGGAAGATGATGCTTTCAAACTCATCTCTGAAAAAAAA	M A A M S E D S C V N F K E M M F I D ACGCTTTACTTTATACCTGAAGAAAATGGAGACCTGGAATCAGACAACTTTGGCCGA T L Y F I P E E N G D L E S D N F G R CACTGTACAACCGCAGTAATACGGAATATAAATGACCAAGTTCTCTTCGTTGACAAA H C T T A V I R N I N D Q V L F V D K CAGCCTGTGTTCGAGGATATGACTGATATTGATCAAAGTGCCAGTGAACCCCAGACC Q P V F E D M T D I D Q S A S E P Q T CTGATAATATACATGTACAAAGACAGTGAAGTAAGAGGACTGGCTGTGACCCTCTCT L I I Y M Y K D S E V R G L A V T L S AAGGATAGTAAAATGTCTACCCTCTCTGTAAGAACAAGATCATTTCCTTTGAGGAA K D S K M S T L S C K N K I I S F E E GATCCACCTGAAAATATTGATGATATACAAAGTGATCTCATATTCTTTCAGAAACGT D P P E N I D D I Q S D L I F F Q K R CCAGGACACAACAAGATGGAGTTTGAATCTTCACTGTATGAAGGACACTTTCTTGCT P G H N K M E F E S S L Y E G H F L A CAAAAGGAAGATGATGCTTTCAAACTCATTCTGAAAAAAAA	ACGCTTTACTTTATACCTGAAGAAAATGGAGACCTGGAATCAGACAACTTTGGCCGACTT T L Y F I P E E N G D L E S D N F G R L CACTGTACAACCGCAGTAATACGGAATATAAATGACCAAGTTCTCTTCGTTGACAAAAGA H C T T A V I R N I N D Q V L F V D K R CAGCCTGTGTTCGAGGATATGACTGATATTGATCAAAGTGCCAGTGAACCCCAGACCAGA Q P V F E D M T D I D Q S A S E P Q T R CTGATAATATACATGTACAAAGACAGTGAAGTAAGAGGACTGGCTGTGACCCTCTCTGTG L I I Y M Y K D S E V R G L A V T L S V AAGGATAGTAAAATGTCTACCCTCTCCTGTAAGAACAAGATCATTTCCTTTGAGGAAATG K D S K M S T L S C K N K I I S F E E M GATCCACCTGAAAATATTGATGATATACAAAGTGATCTCATATTCTTTCAGAAACGTGTT D P P E N I D D I Q S D L I F F Q K R V CCAGGACACAACAAGATGGAGTTGAATCTTCACTGTATGAAGGACACTTTCTTGCTTG

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Ubiquitin

(DNA Sequence, SEQ ID NO: 9; Protein Sequence, SEQ ID NO: 10)

1	ATG	CAG	ATC	TTC	GTG	AAG	ACC	CTG	ACC	GGC	AAC	ACC	ATC	ACC	CTA	GAG	GTG	GAG	CCC	AGT	60
1	M	Q	Ι	F	v	K	T	L	T	G	K	T	I	T	L	E	v	E	P	s	20
61	GAC	ACC	ATC	:GAG	AAC	GTG	AAG	GCC	AAG	ATC	CAG	GAI	'AAA'	GAG	GGC	ATC	CCC	CCT	GAC	CAG	120
21	D	T	I	E	N	V	ĸ	A	K	I	Q	D	K	E	G	I	P	P	D	Q	40
121	CAG	AGG	CTG	ATC	TTT	'GCC	GGC	AAG	CAG	CTG	GAA	GAT	GGC	CGC	ACC	CTC	TCT	GAT	TAC	AAC	180
41	Q	R	L	I	F	A	G	K	Q	L	E	D	G	R	T	L	S	D	Y	N	60
181	ATC	CAG	AAG	GAG	TCA	ACC	CTG	CAC	CTG	GTC	CTT	'CGC	CTG	AGA	GGT	GGC					228
61	I	0	K	E	S	T	L	н	L	v	T,	R	T,	R	G	G					76